**Supplementary Table Legends**

**Supplementary Table 1:** The information of *C. gigas* and *R. venosa* developmental RNA-Seq samples used in this study.

**Supplementary Table 2:** Raw expression counts of 5,427 orthologs across all the samples in *C. gigas* and *R. venosa*, respectively.

**Supplementary Table 3:** 690 common genes that exhibited specific expression patterns in both *C. gigas* and *R. venosa*.(333 up-regulated; 357 down-regulated)

**Supplementary Table 4:** The enriched GO terms (FDR <0.05) of the up-regulated and down-regulated genes shared by both *C. gigas* and *R. venosa* during larval competence.